Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1. (currently amended) A method for detecting a polynucleotide in a sample ~~a breast tumor~~ , comprising the steps of:

a) providing a probe ~~containing a polynucleotide which comprises the sequence~~ which hybridizes under highly stringent conditions to a nucleic acid sequence given by ~~of~~ SEQ ID NO:1 or a fragment thereof;

b) contacting said sample with said probe ~~to a sample of tissue or tissue extract from a patient under a hybridizing condition to produce a hybridized probe~~ ; and

c) quantifying the level of hybridization ~~with~~ of said probe thereby determining the presence or amount of said polynucleotide in said sample ~~wherein suppressed hybridization compared to control levels indicate the presence of a breast tumor~~.

Claim 2. (currently amended) The method of claim 1 wherein said probe ~~comprises at least about 10 nucleotides~~ comprises a sequence of at least 10 consecutive nucleotides.

Claim 3. (withdrawn) A method for regulating a tumor, comprising the steps of:

a) providing a therapeutic composition comprising a polypeptide having the sequence of SEQ ID NO: 2; and

b) providing said therapeutic composition to said tumor.

Claim 4. (withdrawn) A method for regulating an adverse bodily reaction, comprising the steps of:

a) providing a therapeutic composition comprising a polypeptide having the sequence of SEQ ID NO: 2; and

b) providing said therapeutic composition to the area of adverse reaction.

Claim 5. (withdrawn) A method for detecting a tumor, comprising the steps of:

a) providing an antibody of a polypeptide comprising the sequence of SEQ ID NO: 2 or an antigenic fragment thereof;

b) contacting said probe to a sample of body fluid, tissue or tissue extract from a patient under a binding condition to produce a hybridized probe; and
c) quantifying the level of bound polypeptides.

Claim 6. cancelled

Claim 7. (new) A method for detecting a breast tumor in a subject characterized by an altered level of expression of MEC comprising: (a) contacting a breast sample expressing mRNA polynucleotides with a probe that hybridizes to SEQ ID NO:1 or a complement thereof under stringent conditions; and (b) measuring the hybridization level of said probe to said polynucleotides, wherein reduced or loss of said mRNA expression levels compared to levels in breast samples without tumors surrounding the location of said tumor indicates the presence of a breast tumor in said subject.

Claim 8. (new) The method of claim 7, wherein said measuring step is performed by: Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, or in situ hybridization.

Claim 9. (new) The method of claim 8 wherein said probe comprises a sequence of at least 10 consecutive nucleotides.

Claim 10. (new) The method of claim 8 wherein said probe comprises a sequence of at least 20 consecutive nucleotides.

Claim 11. (new) The method of claim 8 wherein said probe comprises a sequence of at least 50 consecutive nucleotides.

Claim 12. (new) A method for detecting a polynucleotide in a sample, comprising the steps of:
a) determining the level of hybridization of a probe which binds under highly stringent conditions to a nucleic acid sequence given by SEQ ID NO:1 or a complement thereof in said sample thereby determining the presence or amount of said polynucleotide in said sample.

Claim 13. (new) The method of claim 12 wherein said probe comprises a sequence of at least 10 consecutive nucleotides.

Claim 14. (new) The method of claim 12 wherein said probe comprises a sequence of at least 20 consecutive nucleotides.

Claim 15. (new) The method of claim 12 wherein said probe comprises a sequence of at least 50 consecutive nucleotides.

Claim 16. (new) A method for detecting a breast tumor in a patient, comprising the steps of:
a) providing a probe the nucleotide sequence of which consists of SEQ ID NO:1 or a fragment thereof;
b) contacting said probe to a sample of breast tissue or breast tissue extract from said patient under highly stringent conditions to permit hybridization of said probe to mRNA encoding a protein encoded by SEQ ID NO. 1; and
c) quantifying the level of hybridization of said probe to said mRNA wherein reduced or loss of said mRNA expression levels compared to levels in breast tissue adjacent to the location of said sample of breast tissue or breast tissue extract from said patient indicates the presence of a breast tumor in said patient.

Claim 17. (new) The method of claim 16 wherein said fragment comprises a sequence of at least 10 consecutive nucleotides unique to SEQ ID NO. 1.